

**AMENDMENTS TO THE SPECIFICATION**

**Please amend the paragraph bridging pp. 3-4 of the specification as follows:**

Recently, random analysis of cDNA molecules has been intensively carried out to analyze various genes, which are expressed in vivo. The cDNA fragments thus obtained have been entered for databases and published as ESTs (Expressed Sequence Tags, e.g., <http://www.ncbi.nlm.nih.gov/dbEST> the database of published sequences provided by the National Center for Biotechnology Information). However, ESTs are merely sequence information, and it is difficult to predict their functions. ESTs are also arranged in the UniGene database (<http://www.ncbi.nlm.nih.gov/UniGene>), and about 92,000 clusters have been registered until now. However, most of these ESTs have their 5' end nucleotide sequences deleted, and contain no translation initiation site. Therefore it is unlikely that such analysis will directly lead to gene functional analysis such as the analysis of protein functions on the assumption of the determination of mRNA coding regions and the understanding of gene expression control by the analysis of promoters.